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(54) **New embodiments of the HIV principal neutralizing determinant.**

(57) **New amino acid sequences of an envelope fragment of HIV are disclosed, as well as immunological conjugates for immunological purposes, including vaccination against AIDS.**

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Acquired Immune Deficiency Syndrome (AIDS) is the clinical manifestation of the apparent infection of CD4 helper T-cells and other cell targets by human immunodeficiency virus (HIV), also previously referred to as human T-lymphotropic virus type III (HTLV-III), Lymphadenopathy-associated virus (LAV), or AIDS-related virus (ARV) (hereinafter collectively "HIV"). AIDS is a transmissible deficiency of cellular immunity characterized by opportunistic infections and certain malignancies. A similar disease, AIDS-related complex (ARC), shares many of the epidemiological features and immune abnormalities with AIDS, and often precedes the clinical manifestations of AIDS.

A vaccine against AIDS and/or ARC is an ideal prophylactic treatment for preventing the debilitating effects of infection by HIV. Applicants have discovered new immunogens useful for such a vaccine. The immunogens are new principal neutralizing determinants (PNDs) of HIV.

Many of the details of the genetic function and virion structure of HIV have not yet been elucidated. However, certain general features have emerged. An RNA virus with a genome totaling about 9 kilobases (kb), its nucleotide sequence contains seven major open reading frames (ORFs) corresponding to the gag, pol and env, vif, tat, rev, and nef genes. The genes gag, pol and env code respectively for core subunits, viral enzymes such as reverse transcriptase or protease, and outer surface subunits. The gene vif codes for a viral infectivity factor, which is a protein involved with enhancement of cell-to-cell transmission of virions without affecting the budding process. The gene tat codes for a small protein that transactivates the expression of all viral proteins. The gene rev regulates expression of the viral proteins of gag, pol and env genes, possibly by facilitating transport of incompletely spliced RNA. The nef gene codes for a viral protein found in the cell cytoplasm, and it may modulate the host cellular signaling system and serve as a transcriptional silencer. Terminal repeats in the nucleotide sequence are common to many retroviruses such as HIV and are required for viral replication and integration into the host chromosome. More recent discussions on the general nature of HIV genomic structure, replication and regulation are found in Ratner, L. et al. "Human T-Lymphotropic Retroviruses," in O'Brien, S.J. (ed.) Genetic Maps 1987 Cold Spring Harbor 1987 pp. 124-129; Franchini, G. et al., Nature 328, 539 (1987); Varmus, H. Genes & Dev 2, 1055 (1988).

Principal neutralizing determinants (PNDs) have been located within a selected, conserved region of the env gene. These PNDs are still undefined. Applicants have discovered and defined new embodiments of PND.

AIDS is a disease of a virus with a unique collection of attributes. HIV itself targets the immune system; it possesses a reverse transcriptase capable of turning out highly mutated progeny; it is sequestered from the immune system and it has a hypervariable surface in the (env) region. See, e.g. Hilleman, M.R., Vaccine 6, 175 (1988); Barnes, D.M., Science 240, 719 (1988). In view of these attributes, it was neither anticipated nor expected that the principal neutralizing determinants of this invention would serve as effective AIDS immunogens.

#### BRIEF DESCRIPTION OF THE INVENTION

New principal neutralizing determinants of HIV are disclosed, and are useful as immunogens for AIDS vaccines, particularly in the form of conjugates

#### ABBREVIATIONS AND DEFINITIONS

AIDS	Acquired immune deficiency syndrome
ARC	AIDS-related complex
conjugation	The process of covalently attaching 2 molecules each containing one or more immunological determinants, e.g., HIV envelope fragments and Omp
conjugate.	Result of conjugation, also known as an antigenic conjugate or immunological conjugate
HIV	Generic term for the presumed etiological agent of AIDS and/or ARC, also referred to as strains HTLV-III, LAV, and ARV.
PND	Principal neutralization determinant of HIV
Omp	Outer membrane proteosome
Recombinant protein	A polypeptide or oligopeptide expressed by foreign DNA in a recombinant eukaryotic or procaryotic expression system.
Recombinant expression system	A cell containing a foreign DNA expressing a foreign protein or a foreign oligopeptide.

Amino Acids		
Full Name	Three-letter symbol	One-letter symbol
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Asn and/or Asp	Asx	B
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Gln and/or Glu	Glx	Z
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

Nucleotides Bases in DNA or RNA	
Name	One-letter symbol
Adenine	A
Cytosine	C
guanine	G
thymine	T
uracil	U

The terms "protein," "peptide," "oligopeptide," and "polypeptide" and their plurals have been used interchangeably to refer to chemical compounds having amino acid sequences of five or more amino acids. "Amino acid" refers to any of the 20 common amino acids for which codons are naturally available, and are listed in the table of amino acids given above.

When any variable (e.g. PND) occurs more than one time in any constituent or in Formula I, its definition on each occurrence is independent of its definition at every other occurrence. Also, combinations of substituents and/or variables are permissible only if such combinations result in stable compounds.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention provides an effective immunogen against AIDS or ARC, and comprises an antigenic conjugate of the formula

(PND)<sub>n</sub>~(Omp) I,

wherein:

PND is the principal neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n = 1-50, wherein n is the number of polypeptides of PND covalently linked to Omp;

~ indicates covalent linkage;

Omp is outer membrane proteosome of the microorganism *Neisseria*;

said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine.

5 The antigenic conjugates of this invention are prepared by isolating and purifying their component parts PND and Omp, then conjugating PND and Omp together. Subsequent purification of conjugate mixtures may be performed as desired.

The new PND amino acid sequences of this invention include any fragment thereof, provided said fragment is at least five amino acids in length.

10 Each PND amino acid sequence is determined by DNA sequencing of HIV clones amplified by the polymerase chain reaction.

#### Polymerase Chain Reaction Amplification

15 Large amounts of DNA coding for PND protein may be obtained using polymerase chain reaction (PCR) amplification techniques as described in Mullis et al., U.S. Patent No. 4,800,159 and other published sources. See also, for example, Innis, M.A. et al. PCR Protocols Academic Press 1990. The extension product of one primer, when hybridized to another primer, becomes a template for the synthesis of another nucleic acid molecule.

20 The primer template complexes act as substrate for DNA polymerase which, in performing its replication function, extends the primers. The region in common with both primer extensions, upon denaturation, serves as template for a repeated primer extension.

Taq DNA Polymerase catalyzes primer extension in the amplification process. The enzyme is a thermostable DNA polymerase isolated from *Thermus aquaticus*. Because it stays active through repeated elevations to high denaturation temperatures, it needs to be added only once. Deoxynucleotide triphosphates provide the building blocks for primer extension.

25 The nucleic acid sequence strands are heated until they separate, in the presence of oligonucleotide primers that bind to their complementary strand at a particular site of the template. This process is continued with a series of heating and cooling cycles, heating to separate strands, and cooling to reanneal and extend the sequences. More and more copies of the strands are generated as the cycle is repeated. Through amplification, the coding domain and any additional primer-encoded information such as restriction sites or translation signals (signal sequences, start codons and/or stop codons) is obtained. PCR protocols are often performed at the 100  $\mu$ L scale in 0.5 ml microcentrifuge tubes. The PCR sample may be single- or double-stranded DNA or RNA. If the starting material is RNA, reverse transcriptase is used to prepare first strand cDNA prior to PCR. Typically, nanogram amounts of cloned template, up to microgram amounts of genomic DNA, or 20,000 target copies are chosen to start optimization trials.

35 PCR primers are oligonucleotides, typically 15 to 50 bases long, and are complementary to sequences defining the 5' ends of the complementary template strands. Non-template complementary 5' extensions may be added to primers to allow a variety of useful post amplification operations on the PCR product without significant perturbation of the amplification itself. It is important that the two PCR primers not contain more than two bases complementary with each other, especially at their 3' ends. Internal secondary structure should be avoided in primers.

40 Because Taq DNA Polymerase has activity in the 37-55°C range, primer extension will occur during the annealing step and the hybrid will be stabilized. The concentrations of the primers are preferably equal in conventional PCR and, typically, are in vast excess of the template to be reproduced.

In one typical PCR protocol, each deoxynucleotide triphosphate concentration is preferably about 200  $\mu$ M. The four dNTP concentrations are preferably above the estimated  $K_m$  of each dNTP (10-15  $\mu$ M).

45 Preferably PCR buffer is composed of about 500 mM potassium chloride, 10.0 mM Tris-HCl (pH 8.3 at room temperature), 1.5 mM magnesium chloride, and 0.01% w/v gelatin. In the presence of 0.8 mM total dNTP concentration, a titration series in small increments over the 1.5-to 4-mM range will locate the magnesium concentration producing the highest yield of a specific product. Too little free magnesium will result in no PCR product and too much free magnesium may produce a variety of unwanted products.

50 Preferably, in a 100- $\mu$ L reaction volume, 2.0 to 2.5 units of Taq DNA Polymerase are recommended. The enzyme can be added conveniently to a fresh master mix prepared for a number of reactions, thereby avoiding accuracy problems associated with adding individual 0.5- $\mu$ L enzyme aliquots to each tube. A typical PCR protocol for amplification of the DNA template includes a 1 minute 94°C denaturation step, a 1 minute 37°C primer annealing step, and a 2 minute 72°C primer extension step. This will amplify a 500 base-pair product at least 100,000-fold in 25 cycles.

During DNA denaturation, sufficient time must be allowed for thermal equilibration of the sample. The practical range of effective denaturation temperatures for most samples is 92-95°C, with 94°C being the standard choice.

Primer annealing is usually performed first at 37°C, and the specificity of the product is evaluated. If unwanted bands are observed, the annealing temperature should be raised in subsequent optimization runs. While the primer annealing temperature range is often 37-55°C, it may be raised as high as the extension temperature in some cases. Merging of the primer annealing and primer extension steps results in a two-step PCR process.

Primer extension, in most applications, occurs effectively at a temperature of 72°C and seldom needs optimization. In the two-temperature PCR process the temperature range may be 65-70°C. In situations where enzyme concentration limits amplification in late cycles, the extension is preferably increased linearly with cyclic number. Usually, 25 to 45 cycles are required for extensive amplification (i.e., 1,000,000 fold) of a specific target.

Once the DNA sequence is determined, through conventional and well-known techniques, its amino acid sequence can be deduced by "translating" the DNA sequence. The resulting amino acid sequence having the principal neutralizing determinant of the envelope gene is then employed to synthesize large quantities of PND protein or fragment thereof. Synthesis is performed by organic synthesis or by recombinant expression systems, or both.

## Preparation of Principal Neutralization Determinant

### A. Organic Synthesis of PND:

Standard and conventional methods exist for rapid and accurate synthesis of long peptides on solid-phase supports. Solution-phase synthesis is usually feasible only for selected smaller peptides.

Synthesis on solid-phase supports, or solid-phase synthesis, is most conveniently performed on an automated peptide synthesizer according to e.g., Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al., (eds.), *Synthetic Peptides in Biology and Medicine*, Elsevier 1985, pp. 29-57. Manual solid-phase synthesis may be employed instead, by following the classical Merrifield techniques, as described, for example, in Merrifield, R.B. J. Am. Chem. Soc. 85, 2149 (1963), or known improvements thereof. Solid-phase peptide synthesis may also be performed by the Fmoc method, which employs very dilute base to remove the Fmoc protecting group. Segment synthesis-condensation is a further variant of organic synthesis of peptides as within the scope of the techniques of the present invention.

In organic synthesis of peptides, protected amino acids are condensed to form amide or peptide bonds with the N-terminus of a growing peptide. Condensation is usually performed with the carbodiimide method by reagents such as dicyclohexylcarbodiimide, or N-ethyl, N<sub>1</sub>-(γ-dimethylaminopropyl) carbodiimide. Other methods of forming the amide or peptide bond include, but are not limited to, synthetic routes via an acid chloride, azide, mixed anhydride or activated ester. Common solid-phase supports include polystyrene or polyamide resins.

The selection of protecting groups of amino acid side chains is, in part, dictated by particular coupling conditions, in part by the amino acid and peptide components involved in the reaction. Such amino-protecting groups ordinarily employed include those which are well known in the art, for example, urethane protecting substituents such as benzyloxycarbonyl (carbobenzoyl), p-methoxycarbobenzoxy, p-nitrocarbobenzoyl, t-butyloxycarbonyl, and the like. It is preferred to utilize t-butyloxycarbonyl (BOC) for protecting the ε-amino group, in part because the BOC protecting group is readily removed by relatively mild acids such as trifluoroacetic acid (TFA), or hydrogen chloride in ethyl acetate.

The OH group of Thr and Ser may be protected by the Bzl (benzyl) group and the ε-amino group of Lys may be protected by the isopropoxycarbonyl (IPOC) group or the 2-chlorobenzyloxycarbonyl (2-Cl-CBZ) group. Treatment with HF or catalytic hydrogenation are typically employed for removal of IPOC or 2-Cl-CBZ.

For preparing cocktails of closely related peptides, see, e.g., Houghton, R.A., *Proc. Natl. Acad. Sci. USA* 82, 5131 (1985).

### B. Expression of PND in a Recombinant Expression System

It is now a relatively straightforward technology to prepare cells expressing a foreign gene. Such cells act as hosts and include *E. coli*, *B. subtilis*, yeasts, fungi, plant cells or animal cells. Expression vectors for

many of these host cells have been isolated and characterized, and are used as starting materials in the construction, through conventional recombinant DNA techniques, of vectors having a foreign DNA insert of interest. Any DNA is foreign if it does not naturally derive from the host cells used to express the DNA insert. The foreign DNA insert may be expressed on extrachromosomal plasmids or after integration in whole or in part in the host cell chromosome(s), or may actually exist in the host cell as a combination of more than one molecular form. The choice of host cell and expression vector for the expression of a desired foreign DNA largely depends on availability of the host cell and how fastidious it is, whether the host cell will support the replication of the expression vector, and other factors readily appreciated by those of ordinary skill in the art.

The technology for recombinant procaryotic expression systems is now old and conventional. The typical host cell is *E. coli*. The technology is illustrated by treatises such as Wu, R (ed) *Meth. Enzymol.* 68 - (1979) and Maniatis, T. et. al., *Molecular Cloning: A Laboratory Manual* Cold Spring Harbor 1982.

The foreign DNA insert of interest comprises any DNA sequence coding for a PND (or fragment thereof of at least 5 amino acids in length) of the present invention, including any synthetic sequence with this coding capacity or any such cloned sequence or combination thereof. For example, PND peptide coded and expressed by an entirely recombinant DNA sequence is encompassed by this invention.

Vectors useful for constructing eukaryotic expression systems for the production of recombinant PND comprise the DNA sequence for PND, fragment or variant thereof, operatively linked thereto with appropriate transcriptional activation DNA sequences, such as a promoter and/or operator. Other typical features may include appropriate ribosome binding sites, termination codons, enhancers, terminators, or replicon elements. These additional features can be inserted into the vector at the appropriate site or sites by conventional splicing techniques such as restriction endonuclease digestion and ligation.

Yeast expression systems, which are one variety of recombinant eukaryotic expression systems, generally employ *Saccharomyces cerevisiae* as the species of choice for expressing recombinant proteins. *S. cerevisiae* and similar yeasts possess well known promoters useful in the construction of yeast expression systems, including but not limited to GAP491, GAL10, ADH2, and alpha mating factor.

Yeast vectors useful for constructing recombinant yeast expression systems for expressing PND include, but are not limited to, shuttle vectors, cosmid plasmids, chimeric plasmids, and those having sequences derived from 2-micron circle plasmids.

Insertion of the appropriate DNA sequence coding for PND, fragment or variant thereof, into these vectors will, in principle, result in a useful recombinant yeast expression system for PND where the modified vector is inserted into the appropriate host cell, by transformation or other means.

Recombinant mammalian expression systems are another means of producing the recombinant PND for the conjugates of this invention. In general, a host mammalian cell can be any cell that has been efficiently cloned in cell culture. Host mammalian cells useful for the purposes of constructing a recombinant mammalian expression system include, but are not limited to, Vero cells, NIH3T3, GH3, COS, murine C127 or mouse L cells. Mammalian expression vectors can be based on virus vectors, plasmid vectors which may have SV40, BPV or other viral replicons, or vectors without a replicon for animal cells. Detailed discussions on mammalian expression vectors can be found in the treatises of Glover, D.M. (ed.) "DNA Cloning: A Practical Approach," IRL 1985, Vols. I and II.

Recombinant PND may possess additional and desirable structural modifications not shared with the same organically synthesized peptide, such as adenylation, carboxylation, glycosylation, hydroxylation, methylation, phosphorylation or myristoylation. These added features may be chosen or preferred as the case may be, by the appropriate choice of recombinant expression system. On the other hand, recombinant PND may have its sequence extended by the principles and practice of organic synthesis of section A above.

#### Conjugation of PND and Omp to Form a Covalent Linkage(s) Yielding Conjugate

Antigenic conjugates of PND and Omp are useful for vaccination against AIDS or ARC. Such conjugates have at least one covalent linkage between the antigen PND and Omp, and typically have more than one PND molecule covalently bound to each Omp molecule.

PND and Omp are prepared separately, then linked by non-specific cross-linking agents, monogeneric spaces or bigeneric spacers. Methods for non-specific cross-linking include, but are not limited to, reaction with glutaraldehyde; reaction with N-ethyl-N'-(3-dimethylaminopropyl) carbodiimide, with or without admixture of a succinylated carrier; periodate oxidation of glycosylated substituents followed by coupling to free amino groups of a protein carrier in the presence of sodium borohydride or sodium cyanoborohydride; diazotization of aromatic amino groups followed by coupling on tyrosine side chain residues of the protein;

reaction with isocyanates; or reaction of mixed anhydrides. See, generally, Briand, J.P. et al. *J. Imm. Meth.* 78, 59 (1985). These methods of non-specifically cross-linking are conventional and well-known in the typical practice of preparing conjugates for immunological purposes.

In another embodiment of the invention conjugates formed with a monogeneric spacer are prepared. These spacers are bifunctional and require functionalization of only one of the partners of the reaction pair to be conjugated before conjugation takes place.

By way of illustration rather than limitation, an example of a monogeneric spacer involves coupling the polypeptide PND to one end of the bifunctional molecule adipic acid dihydrazide in the presence of carbodiimide. A diacylated hydrazine presumably forms with pendant glutamic or aspartic carboxyl groups of PND. Conjugation then is performed by a second coupling reaction with carrier protein in the presence of carbodiimide. For similar procedures, see for example, Schneerson, R. et al., *J. Exp. Med.* 152, 361 (1980). Another example of a monogeneric spacer is described in Fujii, N. et al. *Int. J. Peptide Protein Res.* 26, 121 (1985).

In another embodiment of the invention conjugates of PND and Omp are formed with a bigeneric spacer. These spacers are formed after each partner of the reaction pair to be conjugated, e.g., PND and Omp, is functionalized with a bifunctional spacer. Conjugation occurs when each functionalized partner is reacted with its opposite partner to form a stable covalent bond or bonds. See, for example, Marburg, S. et al., *J. Am. Chem. Soc.* 108, 5282-5287 (1986) and Marburg, S. et al., U.S. Patent 4,695,624, issued 22 September 1987, each incorporated by reference. Bigeneric spacers are preferred for preparing conjugates in human vaccines since the conjugation reaction is well characterized and easily controlled.

Typical and conventional immunological practice provides for the ready and easy synthesis of antigenic conjugates within the scope of the present invention, including the conjugation of Omp with virtually any desired degree of substitution of virtually any peptide of the Sequence Listing. Heterogeneous products of the conjugation reaction are easily separable if needed by a variety of suitable column chromatography techniques.

#### Vaccine Formulation

The form of the immunogen within the vaccine takes various molecular configurations. A single molecular species of the antigenic conjugate (PND)<sub>n</sub>-Omp will often suffice as a useful and suitable antigen for the prevention or treatment of AIDS or ARC. Other antigens in the form of cocktails are also advantageous, and consist of a mixture of conjugates that differ by, for example, the degree of substitution (n) or the amino acid sequence of PND or both.

An immunological vector or adjuvant may be added as an immunological vehicle according to conventional immunological testing or practice.

The conjugates of this invention when used as a vaccine, are to be administered in immunologically effective amounts. Dosages of between 1 µg and 500 µg of conjugate, and preferably between 50 µg and 300 µg of conjugate are to be administered to a mammal to induce anti-peptide, anti-HIV, or HIV-neutralizing immune responses. About two weeks after the initial administration, a booster dose may be administered, and then again whenever serum antibody titers diminish. The conjugate should be given intramuscularly at a concentration of between 10 µg/ml and 1 mg/ml, and preferably between 50 and 500 µg/ml, in a volume sufficient to make up the total required for immunological efficacy.

Adjuvants may or may not be added during the preparation of the vaccines of this invention. Alum is the typical and preferred adjuvant in human vaccines, especially in the form of a thixotropic, viscous, and homogeneous aluminum hydroxide gel. For example, one embodiment of the present invention is the prophylactic vaccination of patients with a suspension of alum adjuvant as vehicle and a cocktail of (PND)<sub>n</sub>-Omp as the selected set of immunogens or antigens.

The vaccines of this invention may be effectively administered, whether at periods of pre-exposure and/or post-exposure, in combination with effective amounts of the AIDS antivirals, immunomodulators, anti-infectives, or vaccines of Table I.

TABLE IANTI-VIRALS

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
AL-721	Ethigen (Los Angeles, CA)	ARC, PGL HIV positive, AIDS
Recombinant Human Interferon Beta	Triton Biosciences (Alameda, CA)	AIDS, Kaposi's sarcoma, ARC
Acemannan	Carrington Labs (Irving, TX)	ARC (See also immuno- modulators)
Cytovene Ganciclovir	Syntex (Palo Alto, CA)	sight threatening CMV peripheral CMV retinitis
d4T Didehydrodeoxy- thymidine	Bristol-Myers (New York, NY)	AIDS, ARC
dd Dideoxyinosine	Bristol-Myers (New York, NY)	AIDS, ARC
EL10	Elan Corp, PLC (Gainesville, GA)	HIV infection (See also immuno- modulators)
Foscarnet Trisodium Phosphonoformate	Astra Pharm. Products, Inc. (Westborough, MA)	CMV retinitis, HIV infection, other CMV infections



	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	Dideoxycytidine; ddc	Hoffman-La Roche (Nutley, NJ)	AIDS, ARC
10	Novapren	Novaferon Labs, Inc. (Akron, OH)	HIV inhibitor
		Diapren, Inc. (Roseville, MN, marketer)	
15	Peptide T Octapeptide Sequence	Peninsula Labs (Belmont, CA)	AIDS
20	Retrovir Zidovudine; AZT	Burroughs Wellcome (Rsch. Triangle Park, NC)	AIDS, adv, ARC pediatric AIDS, Kaposi's sarcoma, asymptomatic HIV infection, less severe HIV disease, neurological involve- ment, in combination w/other therapies, post-exposure pro- phylaxis in health care workers
25			
30			
35			
40	Rifabutin Ansamycin LM 427	Adria Laboratories (Dublin, OH) Erbamont (Stamford, CT)	ARC
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<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
Dextran Sulfate	Ueno Fine Chem. Ind. Ltd. (Osaka, Japan)	AIDS, ARC, HIV positive asymptomatic

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Virazole	Viratek/ICN	asymptomatic HIV
Ribavirin	(Costa Mesa, CA)	positive, LAS, ARC

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Alpha Interferon	Burroughs Wellcome (Rsch. Triangle Park, NC)	Kaposi's sarcoma, HIV in combination w/Retrovir
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Immuno-modulators

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<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
Antibody which neutralizes pH labile alpha aber- rant Interferon in an immuno- adsorption column	Advanced Biotherapy Concepts (Rockville, MD)	AIDS, ARC

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AS-101	Wyeth-Ayerst Labs. (Philadelphia, PA)	AIDS
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Bropirimine	Upjohn (Kalamazoo, MI)	advanced AIDS
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Acemannan	Carrington Labs, Inc. (Irving, TX)	AIDS, ARC (See also anti- virals)
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	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	CL246,738	American Cyanamid (Pearl River, NY) Lederle Labs (Wayne, NJ)	AIDS, Kaposi's sarcoma
10	EL10	Elan Corp, PLC (Gainesville, GA)	HIV infection (See also anti- virals)
15	Gamma Interferon	Genentech (S. San Francisco, CA)	ARC, in combination w/TNF (tumor necrosis factor)
20	Granulocyte Macrophage Colony Stimulating Factor	Genetics Institute (Cambridge, MA) Sandoz (East Hanover, NJ)	AIDS
25			
30	Granulocyte Macrophage Colony Stimulating Factor	Hoeschst-Roussel (Somerville, NJ) Immunex (Seattle, WA)	AIDS
35			
40	Granulocyte Macrophage Colony Stimulating Factor	Schering-Plough (Madison, NJ)	AIDS AIDS, in combination w/Retrovir
45	HIV Core Particle Immunostimulant	Rorer (Ft. Washington, PA)	seropositive HIV

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	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	IL-2 Interleukin-2	Cetus (Emerycille, CA)	AIDS, in combaintion w/Retrovir
10	IL-2 Interleukin-2	Hoffman-La Roche (Nutley, NJ)	AIDS, ARC, HIV, in combination w/Retrovir
15	Immune Globulin Intravenous (human)	Cutter Biological (Berkeley, CA)	pediatric AIDS, in combination w/Retrovir
20	IMREG-1	Imreg (New Orleans, LA)	AIDS, Kaposi's sarcoma, ARC, PGL
25	IMREG-2	Imreg (New Orleans, LA)	AIDS, Kaposi's sarcoma, ARC, PGL
30	Imuthiol Diethyl Dithio Carbamate	Merieux Institute (Miami, FL)	AIDS, ARC
35	INTRON A Alpha-2 Interferon	Schering Plough (Madison, NJ)	Kaposi's sarcoma w/Retrovir: AIDS
40	Methionine- Enkephalin MTP-PE Muramyl- Tripeptide	TNI Pharmaceutical (Chicago, IL) Ciba-Geigy Corp. (Summit, NJ)	AIDS, ARC  Kaposi's sarcoma

	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	Granulocyte Colony Stimulating Factor	Amgen (Thousand Oaks, CA)	AIDS, in combination w/Retrovir
10	rCD4 Recombinant Soluble Human CD4	Genentech (S. San Francisco, CA)	AIDS, ARC
15	Recombinant Soluble Human CD4	Biogen (Cambridge, MA)	AIDS, ARC
20	Roferon-A Interferon Alfa 2a	Hoffman-La Roche (Nutley, NJ)	Kaposi's sarcoma AIDS, ARC, in combination w/Retrovir
25	SK&F106528 Soluble T4	Smith, Kline & French Laboratories (Philadelphia, PA)	HIV infection
30	Thymopentin	Immunobiology Research Institute (Annandale, NJ)	HIV infection
35	Tumor Necrosis Factor; TNF	Genentech (S. San Francisco, CA)	ARC, in combina- tion w/gamma Interferon
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Anti-Infectives

	<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
5	Clindamycin with Primaquine	Upjohn (Kalamazoo, MI)	PCP
10	Diflucan Fluconazole	Pfizer (New York, NY)	cryptococcal meningitis, candidiasis
15	Pastille Nystatin Pastille	Squibb Corp. (Princeton, NJ)	prevention of oral candidiasis
20	Ornidyl Eflornithine	Merrell Dow (Cincinnati, OH)	PCP
25	Pentamidine Isethionate (IM & IV)	LyphoMed (Rosemont, IL)	PCP treatment
30	Piritrexim	Burroughs Wellcome (Rsch. Triangle Park, NC)	PCP treatment
35	Pentamidine isethionate for inhalation	Fisons Corporation (Bedford, MA)	PCP prophylaxis
40	Spiramycin	Phone-Poulenc Pharmaceuticals (Princeton, NJ)	cryptosporidial diarrhea
45			
50			
55			

<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
Intraconazole- R51211	Janssen Pharm. (Piscataway, NJ)	histoplasmosis; cryptococcal meningitis
Trimetrexate	Warner-Lambert	PCP
<u>Other</u>		
<u>Drug Name</u>	<u>Manufacturer</u>	<u>Indication</u>
Recombinant Human Erythropoietin	Ortho Pharm. Corp. (Raritan, NJ)	severe anemia assoc. and Retrovir therapy
Megestrol Acetate	Bristol-Myers (New York, NY)	treatment of anorexia assoc. w/AIDS
Total Enteral	Norwich Eaton Pharmaceuticals (Norwich, NY)	diarrhea and malabsorption related

It will be understood that the scope of combinations of the antigenic conjugates of this invention with AIDS antivirals, immunomodulators, anti-infectives or vaccines is not limited to the list in the above Table, but includes in principle any combination with any pharmaceutical composition useful for the treatment of AIDS. The antigenic conjugates as AIDS or HIV vaccines of this invention include vaccines to be used pre- or post-exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen.

#### EXAMPLE 1

##### Isolation of Genomic DNA from Frozen (-20° C) Pellets of Peripheral Blood Lymphocytes

Each DNA was prepared respecting the principle that preparation and storage of high molecular weight DNA be segregated from all polymerase chain reaction (PCR) amplification experiments.

Reagents

## P-K Buffer

5      10 mM Tris  
      400 mM NaCl    pH 7.4  
      2 mM EDTA

Prepare using sterile H<sub>2</sub>O in plastic labware. Sterile filter through a 0.45 µm filter device and aliquot 10 ml into 15 ml conical tubes. Store at -20°C.

15    Proteinase K    1.0mg/ml

Dissolve the contents of a bottle in sterile H<sub>2</sub>O to a final conc. of 1.0 mg/ml. Aliquot 0.3-0.5 ml into freezer tubes. Store at -20°C.

25    SDS 10%

Prepare using sterile H<sub>2</sub>O in plastic labware. Sterile filter through a 0.45 µm filter device and aliquot 2.0 ml into Nalgene freezer tubes. Store at -20°C.



Phenol:Chloroform 50:50 Prepare and aliquot 8.0 ml into  
15 ml conical tubes and store at  
-20°C in the dark.

RNase A 1.0 mg/ml Dissolve the contents of a bottle  
in sterile H<sub>2</sub>O to a final  
conc. of 1.0 mg/ml. Aliquot 0.3-  
0.5 ml into freezer tubes. Store  
at -20°C.

95% and 70% EtOH Store at -20°C.

Dilution Buffer Prepare using sterile H<sub>2</sub>O in  
plastic labware. Sterile filter  
through a 0.45 µm filter device  
and aliquot 10 ml in 15 ml  
conical tubes. Store at 4°C.

- 1) Suspend cell pellets of co-cultivated patient peripheral blood lymphocytes in 0.5 ml of P-K Buffer taking care to break up pellet completely.
- 2) Adjust sample to 100 µg/ml Proteinase K with 1.0 mg/ml stock. Mix well.
- 3) Adjust sample to 0.5% SDS with 10% stock. Mix well and incubate at 50°C for 16-24 hours.
- 4) Extract sample with an equal volume of Phenol: Chloroform for 10 minutes @ 21-25°C.
- 5) Split phases by centrifugation @ 2K for 5 minutes.
- 6) Remove aqueous and re-extract with an equal vol. of CHCl<sub>3</sub> for 2-5 minutes @ 21-25°C. Split phases as before.
- 7) Repeat Step 6.
- 8) Adjust aqueous to 100 µg/ml RNase A with 1.0 mg/ml stock and incubate @ 37°C for 90 minutes.
- 9) Repeat Steps 4, 5, 6, and 7.
- 10) Precipitate DNA with the addition of 2.5 vol of cold 95% EtOH.
- 11) Collect DNA for 30 minutes at 10,000 RPM's at 4°C.
- 12) Remove EtOH and wash pellet once with 70% EtOH. Spin for 2 minutes as 10,000 RPM's.
- 13) Remove EtOH and dissolve the pellet in 300µl of dilution buffer.

## EXAMPLE 2

### PCR Amplification of Genomic DNA from HIV Isolates

Genomic DNA was amplified by the polymerase chain reaction according to Scharf, S.J. et al. Science 233, 1076 (1986). A heat resistant *T. aquaticus* DNA polymerase was employed to enhance stability during thermal cycling. See, e.g., Saiki, R. K. et al. Science 239, 487 (1988). Excess primer for each strand was used. The primers were

RP.Hpa having the sequence

5'-P-TCT-GTT-AAC-TTC-ACA-GAC-AAT-GCT-AAA-ACC-ATA-ATA-GTA-CAG-CTG-3'; and

RP.Cla having the sequence

5'-P-GCA-ATC-GAT-CTG-TTT-TAA-AGT-GTT-ATT-CCA-TTT-TGC-3'

The 5' phosphate was added by chemical methods, according to Horn, T. et al., Tetrahedron Letters 27, 4705 (1986).

**EXAMPLE 3****Filtration of PCR Amplified Sequences****5    General Considerations:**

This filtration step removes free nucleotides and low molecular weight oligonucleotide contaminants which inhibit ligation, according to Sharf, et al. Science, 233, 1076 (1986).

10    1) Dilute up to 100 $\lambda$  of sample (1-2  $\mu$ g DNA/ml) of Example 2 to 400 $\lambda$  with "buffer" (10 mM Tris $\cdot$ HCl, 25 mM NaCl, 0.1 mM EDTA, all buffered to pH8) and spin in a microcentrifuge for 5 minutes at RT.

N.B. No more than 4 samples can be placed in same rotors at one time. Be sure that the cap of the tube is completely closed or some volume may spray out of the unit. If using a non-dedicated microcentrifuge, spin sample at 2000 x g.

15    2) Remove insert and place in a clean 1.5 ml plastic tube containing a polysulfone filter with a 100,000 dalton molecular weight cut off. Redilute sample to 400 $\lambda$  with buffer and spin as before.

3) Repeat Step 2.

4a) For Cloning purposes:

Remove sample and rinse membrane gently with 10-20 $\lambda$  of buffer. Combine the sample and rinse and adjust back to the original volume. Check on agarose gel for yield and purity.

20    4b) For Reamplification purposes:

Remove sample carefully measuring volume. Rinse the membrane gently with additional buffer as above. Adjust back to the original volume (100 $\lambda$ ) and use 5 $\lambda$  of the sample for reamplification.

**EXAMPLE 4**

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**Ligation and Cloning of PCR Amplified Sequences****Reagents**

30

pUC13 SmaI/Bap

A cloning vector  
commercially prepared by  
Pharmacia, dissolved in 10  
mM Tris pH8.0, aliquoted and  
stored at -20°C. Its

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sequence and preparation are described in Vieira, J. et al., Gene 19, 259 (1982), incorporated by reference for these purposes.

5X ligation buffer prepared from stocks  
 250 mM Tris pH7.8 aliquoted and stored at  
 50 mM  $MgCl_2$   $-20^{\circ}C$ .  
 100 mM DTT  
 5.5 mM ATP  
 250 mg/ml BSA

$T_4$  DNA Ligase New England Biolabs

SOC media

25

Final  
Concentration

30	Bactotryptone	2%	- To 97 ml distilled $H_2O$ , add bacto-tryptone, yeast extract, NaCl and KCl. Stir to dissolve, autoclave, and cool to room temperature. Make medium 20 mM in $Mg^{++}$ stock with a 2 M $Mg^{++}$ (1 M $MgCl_2 \cdot 6H_2O$ + 1 M $MgSO_4$ ).
	Yeast Extract	0.5%	
	NaCl	10 mM	
35	KCl	2.5 mM	
	$MgCl_2$ , $MgSO_4$	20 mM (10 mM each)	
	Glucose	20 mM	
40	Distilled $H_2O$	----	

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7H<sub>2</sub>O, filter-sterilized). Add 2<sup>4</sup>M glucose stock (filter-sterilized) to make the medium 20 mM final. Filter the complete medium through a 0.2 - µm filter unit. pH should be 7.0 ± 0.1. Filter-sterilizing units should be pre-filtered with distilled H<sub>2</sub>O before use to remove any toxic material from the filter.

Luria Bertani Agar + 100 µg/ml

Ampicillin - commercially prepared from REMEL. For composition, see Sambrook, J. et al., Molecular Cloning 3, A.1 (2nd.Ed., 1989)

Xgal 2% in dimethyl-formamide

- stored at -20°C. Xgal is 5-bromo-4-chloro-3-indolyl β-D-galactoside.

IPTG 100 mM in H<sub>2</sub>O

- stored at -20°C. IPTG is isopropyl-thiogalactoside.

- 1). Combine 10λ of filtered PCR amplified DNA (10-20 ng/ml) with 20 ng of pUC13 SmaI/BAP and 100 units of T<sub>4</sub> DNA ligase in a final volume of 20λ.
- 2). Incubate at 21-25° C for 3 hours.
- 3). Transform 100λ of transformation competent bacteria using 10λ of ligation buffer.
- 4). Incubate on ice for 30 minutes in sample tubes.

- 5). Heat shock tubes for 45 seconds at 42° C.
- 6). Reincubate on ice for 2 minutes before adding 1.0 ml of SOC media (21-25° C).
- 7). Incubate 1 hour at 37° C shaking at 225 RPM's.
- 8). Pellet cells in 1.5 ml plastic tubes for 10 seconds at maximum speed.
- 9). Remove the media except about 100 $\lambda$ . Care should be taken removing the media as the pellet is loose.
- 10). Resuspend the cells in the remaining 100 $\lambda$  and spread on an L agar plate containing Ampicillin and onto which 100 $\lambda$  of Xgal and 50 $\lambda$  of IPTG had been previously spread.
- 11). Invert the incubate at 37° C. Colonies are visible after 12 hours. Blue color indication is clear after 16 hours.

#### EXAMPLE 5

##### Isolation of Plasmid DNA for Subsequent Dideoxy Sequence Analysis

#### Reagents

##### MP Buffer 1

50 mM Glucose  
10 mM EDTA  
25 mM Tris pH 8.0

##### MP Buffer 2 - made fresh for each experiment

0.2 N NaOH  
1% SDS

##### MP Buffer 3

Potassium Acetate pH ~5.6  
60 ml 5M KOAc  
28.5 ml H<sub>2</sub>O  
11.5 ml gl. HOAc

##### RNase Stock

1.0 mg/ml RNase A dissolved in H<sub>2</sub>O and boiled  
10 minutes

##### Phenol:Chloroform (50:50)

Phenol is buffer saturated with an equal volume of buffer (50 mM Tris·HCl, 100 mM NaCl, 1mM EDTA, pH 8.0)

##### PEG

13% Poly Ethylene Glycol (PEG-8000)

##### 4M NaCl

95% and 70% EtOH

- 1). Three individual colonies from each isolate are selected at random and placed in 10 ml of L Broth. Each are grown overnight in a 50 ml conical tube shaking @ 225-250 RPM's @ 37° C.
- 2). Collect 9.5 ml of overnight culture at 1K for 20 minutes.
- 3). Dry pellet well and resuspend by vortexing in 200 $\lambda$  of MP 1. Transfer to a 1.5 ml plastic tube. Incubate 5 minutes @ RT.

- 4). Add 40 $\lambda$  of MP 2 and incubate 5 minutes on ice. Mix by inversion.
- 5). Add 300 $\lambda$  of MP 3 and incubate 5 minutes on ice. Mix by inversion.
- 6). Centrifuge 10,000 Xg for 5 minutes @ 4° C.
- 7). Transfer supernatant to a fresh 1.5 ml tube and add 10 $\lambda$  of a 1.0  $\mu$ g/ml RNase A stock. Incubate 30 minutes @ 37° C.
- 8). Extract with an equal volume (-500 $\lambda$ ) of buffer saturated phenol:chloroform. Split phases.
- 9). Transfer aqueous to a fresh tube and precipitate by adding 1.0 ml of cold EtOH. Incubate @ -70° C for 30 minutes.
- 10). Collect at full speed (about 10,000 Xg) for 15 minutes @ 4° C.
- 11). Remove EtOH and wash with 1.0 ml cold 70% EtOH. Respin for 2 minutes.
- 12). Remove EtOH and drain tube well. Dry pellet by inversion and then redissolve in 80 $\lambda$  H<sub>2</sub>O.
- 13). Adjust sample with 20 $\lambda$  4M NaCl and 100 $\lambda$  PEG. Incubate 30 minutes on ice.
- 14). Centrifuge at full speed (about 10,000 Xg) for 15 minutes @ 4° C.
- 15). Remove supernatant and wash pellet with 1.0 ml cold 70% EtOH. Respin for 2 minutes.
- 16). Remove EtOH and drain tube well. Dry pellet in speed vac. and then redissolve in 20 $\lambda$  H<sub>2</sub>O.

EXAMPLE 6DETERMINATION OF THE DNA SEQUENCE

Sequencing was performed by the method of Tabor, S. et al., Proc. Nat. Acad. Sci., 84, 4767 (1987). Sequencing gels were read and checked with a scanner. Amino acid sequences were deduced from DNA.

EXAMPLE 7Preparation of Synthetic Peptides

A. The oligopeptide EE15-1 of the sequence:

1	5	10	15
Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly			
TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA			
20	25	30	
Pro Gly Arg Ala Leu Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile			
CCA GGG AGA GCA CTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA			
35			
Arg Arg Ala Tyr Cys			
AGA CGA GCA TAT TGT			

is synthesized by conventional solid-phase techniques on an automated peptide synthesizer, according to Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al. (eds.), Synthetic Peptides in Biology and Medicine, Elsevier 1985, pp. 29-57.

B. Each of the peptides of the Sequence Listing is prepared by the same method.

C. Oligopeptide EE15-1 was prepared in a recombinant expression system in E. coli according to the methods of Sambrook, J. et al., Molecular Cloning 3, 17.3 et seq. Cold Spring Harbor 2nd Ed. 1988.

Every other peptide of the Sequence Listing is also prepared in a recombinant expression system in E. coli.

EXAMPLE 8

Extraction and Purification of Omp

## A. First Method

5 All materials, reagents and equipment were sterilized by filtration, steam autoclave or ethylene oxide, as appropriate; aseptic technique was used throughout.

A 300 gm (wet weight) aliquot of 0.5% phenol inactivated cell paste of Meningococcal group B11 was suspended in 1200 mls of distilled water than suspended by stirring magnetically for 20 minutes at room temperature. The suspended cells were pelleted at 20,000 xg for 45 minutes at 5 °C.

10 For extraction, the washed cells were suspended in 1500 mls 0.1 M Tris, 0.01 M EDTA Buffer pH 8.5 with 0.5% sodium deoxycholate (TED Buffer) and homogenized with a 500 ml Sorvall omnimixer at setting 3 for 60 seconds. The resulting suspension was transferred to ten Erlenmeyer flasks (500 ml) for extraction in a shaking water bath for 15 minutes at 56 °C. The extract was centrifuged at 20,000 x g for 90 minutes at 5 °C and the viscous supernatant fluid was decanted (volume = 1500 mls). The decanted fluid was very  
15 turbid and was recentrifuged to clarify further at 20,000 x g for 90 minutes at 5 °C. The twice spun supernatant fluid was stored at 5 °C. The extracted cell pellets were resuspended in 1500 mls TED Buffer. The suspension was extracted for 15 minutes at 56 °C and recentrifuged at 20,000 x g for 90 minutes. The supernatant fluids which contained purified Omp were decanted (volume = 1500 mls) and stored at 5 °C.

## 20 B. Second Method

All material, reagents, equipment and filters were sterilized by heat, filtration or ethylene oxide. One exception was the K-2 ultracentrifuge which was sanitized with a 0.5% formalin solution. Laminar flow canopies provided sterility protection during equipment connections. Aseptic techniques were followed  
25 throughout the entire operations. Overnight storage of the protein was at 2-8 °C between steps. A 0.2 micron sterile filtration was conducted just before the final diafiltration to ensure product sterility.

Two 600-liter batches of *Neisseria meningitidis* were fermented and killed with 0.5% phenol, then concentrated to roughly 25 liters using two 10 ft<sup>2</sup> 0.2 micron polypropylene cross-flow filtration membranes. The concentrated broth then was diafiltered with 125 liters of cell wash buffer (0.11 M Sodium Chloride,  
30 17.6 mM Sodium Phosphate Diabasic, 23.3 mM Ammonium Chloride, 1.34 mM Potassium Chloride, adjusted to pH 7 with 85% Phosphoric Acid followed by 2.03 mM Magnesium Sulfate Heptahydrate).

For extraction, an equal volume of 2X-TED buffer (0.2M Tris, 0.02M EDTA adjusted to pH 8.5 with concentrated HCl followed with the addition of 1.0% sodium deoxycholate) was added to the cell slurry. The resulting slurry was heated to 56 ± 3 °C and maintained at this temperature for 30 minutes to complete the  
35 extraction of Omp from the cells.

For further purification, the extracted cell slurry was centrifuged at 30,000 x g (18,000 rpm) in a "one-pass" flow mode in a K-ultracentrifuge, and the supernatant stream was collected. The low-speed supernatant was concentrated to 10 liters on two 0.1-micron polysulfone autoclavable hollow-fiber membranes and collected in an 18 liter sterile bottle. The filtration equipment was given two 4-liter rinses with  
40 TED buffer (0.1M Tris, 0.01M EDTA, adjusted to pH 8.5 with concentrated HCl, followed with the addition of sodium deoxycholate to 0.5%) which was combined with the retentate. The retentate was subdivided into two or three equal parts. Each part was centrifuged at 80,000 x g (35,000 rpm) for 30 minutes. The Omp protein was pelleted, and the majority of soluble proteins, nucleic acids and endotoxins remained in the supernatant. The supernatant was discarded. The pelleted protein was resuspended by recirculating 55 ±  
45 5 °C TED buffer through the rotor. The first high-speed resuspensions were combined and subjected to a second low-speed spin. The second low-speed spin ensured that residual cell debris was removed from the product stream. The second low speed supernatant was subdivided into two or three equal parts. Each fraction was given two consecutive high-speed spins. All high-speed spins were operated under the same conditions and each further purified the Omp protein.

50 For sterile filtration and final diafiltration, the third high-speed resuspensions were diluted with an equal volume of TED buffer and filtered through a 0.2 micron cellulose acetate filter. When all fractions were permeated, an 8 L TED buffer rinse was used to flush the filtration system. The permeate and rinse were combined and concentrated to 3 liters on a 0.1 micron polysulfone autoclavable hollow fiber membrane. The material then was diafiltered with 15 liters of sterile pyrogen free water. The retentate was collected in a 4-  
55 liter bottle along with a 1-L rinse to give the final product. The final aqueous suspension was stored at 2-8 °C, as purified Omp.

## C. Third Method

Omp is purified from 0.2 M LiCl-0.1M Na Acetate, pH 5.8, extracts by ultracentrifugation, by the method of C.E. Frasch et al. J. Exp. Med. 140, 87-104 (1974), herein incorporated by reference.

#### EXAMPLE 9

##### A. Preparation of (EE15-1 Peptide)-Omp conjugate ("EE15-1-Omp" conjugate)

N-acetylhomocystaminylated outer membrane protein (Omp) of *N. meningitidis* from 59 mg of Omp (purified by Method B of Example 2) is prepared by the centrifugation method described in Marburg, S. et al., J. Am. Chem. Soc. 108:5282 (1986). This material (about 50 mg) is reacted at pH 8 (6.5 mL 0.1M  $\text{PO}_4$  Buffer) with 20 mg of N-D-bromoacetylated EE15-1 (lyophilized) under  $\text{N}_2$  for 18 hours at room temperature.

The reaction mixture is diluted to 10 mL with  $\text{H}_2\text{O}$  and centrifuged for 2h, at 4 °C and 43,000 rpm. The supernatant is removed, and the pellet resuspended, using a Dounce tissue homogenizer, in 10 mL of  $\text{H}_2\text{O}$ . This suspension is recentrifuged (as above) and the pellet resuspended in 9.5 mL of  $\text{H}_2\text{O}$ . A low speed spin for 1 minute in a clinical centrifuge removes a flocculent insoluble material if any. The degree of substitution can be determined and calculated by a variety of methods.

##### B. Preparation of Other Peptide Conjugates

By the method of Example 9A the following peptide-Omp conjugates are obtained:

(EE15-1)<sub>5</sub>-Omp,  
(EE164-3)<sub>4</sub>-Omp,  
(EE244-1)<sub>6</sub>-Omp,  
(EE310-2)<sub>8</sub>-Omp,  
(EE311-1)<sub>10</sub>-Omp,  
(EE359-2)<sub>8.5</sub>-Omp,  
(EE360-1)<sub>3.3</sub>-Omp, and  
(EE543-1)<sub>4.0</sub>-Omp.

#### EXAMPLE 10

##### Protocol for Inoculation of Animals with the (EE15-1)<sub>5</sub>-Omp Conjugate (hereinafter "EE-15-1-Omp" conjugate)

Alum is used as an adjuvant during the inoculation series. The inoculum is prepared by dissolving the EE15-1-Omp conjugate in physiologic saline at a final conjugate concentration of 100 µg/ml. Preformed alum (aluminum hydroxide gel) is added to the solution to a final level of 500 µg/ml aluminum. The conjugate is allowed to adsorb onto the alum gel for two hours at room temperature. Following adsorption, the gel with the conjugate is washed twice with physiologic saline and resuspended in the saline to a protein concentration of about 100 µg/ml.

African green monkeys are individually inoculated with four 100 mcg doses of the EE15-1-Omp conjugate adsorbed onto alum. Each dose is injected intramuscularly. The doses are delivered one or five months apart (week 0, 4, 8 and 28). The animals are bled at intervals of two or four weeks. Serum samples are prepared from each bleed to assay for the development of specific antibodies as described in the subsequent examples.

#### EXAMPLE 11

##### Analysis of Sera for Anti-Peptide IgG Antibodies

Each serum sample is analyzed by enzyme-linked immunoadsorbent assay (ELISA). Polystyrene microtiter plates are coated with 0.5 µg per well of the synthetic peptide (not conjugated to Omp) in phosphate-buffered physiological saline (PBS) at 4 °C. Each well is then washed with PBS containing 0.05% TWEEN-20 (PBS-T). Test serum, diluted serially in PBS-T, is added to the peptide-containing wells and allowed to react with the adsorbed peptide for one hour at 36 °C. After washing with PBS-T, alkaline phosphatase-conjugated goat anti-human IgG is added to the test wells and is allowed to react for one hour at 36 °C. The wells are then washed extensively in PBS-T. Each well receives 0.1% p-nitrophenyl phosphate in 10% diethanolamine, pH 9.8, containing 0.5 mM  $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$ . The ensuing reaction is allowed



to proceed at room temperature for 30 minutes, at which time it is terminated by the addition of 3.0 N NaOH.

The greater the interaction of antibodies in the test serum with the peptide substrate, the greater is the amount of alkaline phosphatase bound onto the well. The phosphatase enzyme mediates the breakdown of p-nitrophenyl phosphate into a molecular substance which absorbs light at a wavelength of 405 nm. Hence, there exists a direct relationship between the absorbance at 405 nm of light at the end of the ELISA reaction and the amount of peptide-bound antibody.

Titers of anti-(EE15-1-Omp) antibody are thus readily determined.

## 10 EXAMPLE 12

### Analysis of Sera for Activity which Specifically Neutralizes HIV Infectivity

Virus-neutralizing activity is determined with an assay described by Robertson et al., J. Virol. Methods 20: 195-202 (1988). The assay measures specific HIV-neutralizing activity in test serum. The assay is based on the observation that MT-4 cells, a human T-lymphoid cell line, are readily susceptible to infection with HIV and, after a period of virus replication, are killed as a result of the infection.

The test serum is treated at 56°C for 60 minutes prior to the assay. This treatment is required to eliminate non-specific inhibitors of HIV replication. Heat treated serum, serially diluted in RPMI-1640 cell culture medium, is mixed with a standard infection dose of HIV. The dose is determined prior to the assay as containing the smallest quantity of virus required to kill all the MT-4 cells in the assay culture after a period of 7 days. The serum-virus mixture is allowed to interact for one hour at 37°C. It then is added to  $1.0 \times 10^5$  MT-4 cells suspended in RPMI-1640 growth medium supplemented with 10% fetal bovine serum. The cultures are incubated at 37°C in a 5% CO<sub>2</sub> atmosphere for 7 days.

At the end of the incubation period, a metabolic dye, DTT, is added to each culture. This dye is yellow in color upon visual inspection. In the presence of live cells, the dye is metabolically processed to a molecular species which yields a blue visual color. Neutralized HIV cannot replicate in the target MT-4 cells and therefore does not kill the cells. Hence, positive neutralization is assessed by the development of blue color following addition of the metabolic dye.

All the monkeys inoculated with the EE15-1-Omp conjugate are bled for specific HIV infectivity-neutralizing activity. Further follow-up evaluation of the same monkeys is also performed. Booster shots are also administered to ascertain renewed neutralizing titer.

While the foregoing specification teaches the principles of the present invention, with examples provided for the purpose of illustration, it will be understood that the practice of the invention encompasses all of the usual variations, adaptations, modifications, deletions or additions of procedures and protocols described herein, as come within the scope of the following claims and its equivalents.

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55

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: J.A. LEWIS ET AL.
- (ii) TITLE OF INVENTION: NEW EMBODIMENTS OF THE  
HIV PRINCIPAL NEUTRALIZING DETERMINANT
- (iii) CORRESPONDENCE ADDRESS: MERCK & CO., INC.  
(A) STREET: P.O. BOX 2000, EAST LINCOLN AVE.  
(B) CITY: RAHWAY  
(C) STATE: NEW JERSEY  
(D) COUNTRY: USA  
(E) ZIP: 07065
- (iv) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette, 5.25 in., 360 Kb storage  
(B) COMPUTER: Wang PC 381  
(C) OPERATING SYSTEM: MS-DOS 3.30.10  
(D) SOFTWARE: Microsoft WORD 5.0
- (v) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: NA  
(B) FILING DATE: NA  
(C) CLASSIFICATION: NA
- (vi) PRIOR APPLICATION DATA: NONE  
(A) DOCUMENT NUMBER: \_\_\_\_\_  
(B) COUNTRY: \_\_\_\_\_  
(C) FILING DATE: \_\_\_\_\_  
(D) PUBLICATION DATE: \_\_\_\_\_
- (vii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: R.D. MEREDITH  
(B) REGISTRATION NUMBER: 30,777  
(C) REFERENCE/DOCKET NUMBER: 18114Y
- (viii) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 201-594-4678  
(B) TELEFAX: 201-594-4720  
(C) TELEX: \_\_\_\_\_
- (ix) PUBLICATION STATUS: NOT KNOWN  
(A) AUTHORS: \_\_\_\_\_  
(B) TITLE: \_\_\_\_\_  
(C) JOURNAL: \_\_\_\_\_  
(D) VOLUME: \_\_\_\_\_  
(E) ISSUE: \_\_\_\_\_  
(F) PAGES: \_\_\_\_\_  
(G) DATE: \_\_\_\_\_  
(H) RELEVANT RESIDUES:  
(1) START: \_\_\_\_\_  
(2) END: \_\_\_\_\_  
(3) BASE PAIRS: \_\_\_\_\_  
(4) AMINO ACIDS: \_\_\_\_\_

(2) INFORMATION FOR SEQ ID NO: EE15-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL

ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE15-1

```

1           5           10           15
Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly
TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA

20           25           30
Pro Gly Arg Ala Leu Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile
CCA GGG AGA GCA CTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

35
Arg Arg Ala Tyr Cys
AGA CGA GCA TAT TGT

```

(2) INFORMATION FOR SEQ ID NO: EE15-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):
  - (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
  - (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE15-2

1	5	10	15
Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly			
TGT ACA AGG CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA			
20	25	30	
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile			
CCA GGG AGA GCC TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA			
25	35		
Arg Gln Ala His Cys			
AGA CAA GCA CAT TGT			
30			

(2) INFORMATION FOR SEQ ID NO: EE15-3

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
  - (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
  - (C) CLONE: \_\_\_\_\_

- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION: SEQ ID NO: \_\_

5

SEQ ID NO: EE15-3

10

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly  
 TGT ACA AGG CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

15

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCC TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

20

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

25

## (2) INFORMATION FOR SEQ ID NO: EEE37-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

30

## (ii) KIND: cDNA to genomic RNA

## (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

35

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

40

## (v) POSITION IN GENOME: Within Env Gene

## (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

## (viii) SEQUENCE DESCRIPTION:

45

50

55

SEQ ID NO: EEE37-1

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Thr MET Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGG ATA ACT ATG GGA  
  
 20 25 30  
 10 Pro Gly Arg Val Phe Tyr Thr Thr Gly Gly Ile Ile Gly Asn Ile  
 CCA GGG AGA GTA TTT TAT ACA ACA GGA GGA ATA ATA GGA AAT ATA  
  
 35  
 15 Arg Arg Ala His Cys  
 AGA CGA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EEE37-2  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EEE37-2

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE37-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE37-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Gly Asp  
 CCA GGA CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA GGA GAT

35  
 Ile Arg Gln Ala His Cys  
 ATA AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE54-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE54-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATC AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EEE69-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA



- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 5 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 10 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EEE69-1

1 5 10 15  
 Cys Thr Arg Leu Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 20 TGT ACA AGG CTC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  
 20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 25 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA  
 30 35  
 Arg Gln Ala His Cys  
 30 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EEE69-2  
 (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 40 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 45 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 50 determinant  
 (viii) SEQUENCE DESCRIPTION:

55

SEQ ID NO: EEE69-2

1 5 10 15  
 5 Cys Thr Arg Leu Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CTC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA  
 35  
 15 Arg Gln Ala Gln Cys  
 AGA CAA GCA CAG TGT

20 (2) INFORMATION FOR SEQ ID NO: EE74-1  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE74-1

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GCA GAT ATA

5  
 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- 10 (2) INFORMATION FOR SEQ ID NO: EE74-2
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

30  
 SEQ ID NO: EE74-2

35 1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

40 20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACC ACA GGA GAC ATA ATA GCA GAT ATA

45 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

50

55

## (2) INFORMATION FOR SEQ ID NO: EE74-3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE74-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EEE90-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

15

SEQ ID NO: EEE90-1

1 5 10 15  
 20 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Ala  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

20 25 30  
 25 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA

30 35  
 30 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE90-2
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

55

SEQ ID NO: EE90-2

```

      1           5           10           15
5  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala
   TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

      20           25           30
10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
   CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA

      35
15 Arg Gln Ala His Cys
   AGA CAA GCA CAT TGT

```

```

(2)  INFORMATION FOR SEQ ID NO: EE90-3
20  (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 105
      (B)  TYPE: Nucleic Acid
      (C)  STRANDEDNESS: Single
      (D)  TOPOLOGY: Linear
25  (ii) KIND: cDNA to genomic RNA
      (ii) KIND (if peptide or protein):
      (A)  SEQUENCE ASSEMBLY METHOD: Overlap
      (B)  FRAGMENT TYPE: Internal Fragment
      (C)  HYPOTHETICAL: _____
30  (iii) ORIGINAL SOURCE: HIV
      (E)  INDIVIDUAL ISOLATE: _____
      (iv) IMMEDIATE SOURCE:
      (C)  CLONE: _____
      (v)  POSITION IN GENOME: Within Env Gene
35  (vi)  PROPERTIES OF SEQUENCE: Expresses conserved antigenic
      determinant
      (viii) SEQUENCE DESCRIPTION:

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SEQ ID NO: EE90-3

```

      1           5           10           15
45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala
   TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

```

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE100-1
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE100-1

1 5 10 15  
 Cys Thr Arg Pro His Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGC ACA AGA CCC CAC AAC AAT ACA AGG AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala Tyr Cys  
 AGA CAA GCA TAT TGT

(2) INFORMATION FOR SEQ ID NO: EEE100-2

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
  - (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (iii) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
  - (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE100-2

1	5	10	15
Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys Ser Ile His Ile Gly			
TGC ACA AGA CCC GGC AAC AAT ACA AGG AAA AGT ATA CAT ATA GGA			

  

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA		

  

35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE100-3

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA



- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 5 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 10 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE100-3

1 5 10 15  
 20 Cys Thr Arg Pro His Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGC ACA AGA CCC CAC AAC AAT ACA AGG AAA AGT ATA CAT ATA GGA

1 5 10 15  
 25 Pro Gly Arg Ala Trp Tyr Thr Thr Gly Ala Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TGG TAT ACA ACA GGA GCA ATA ATA GGA GAT ATA

35  
 30 Arg Gln Ala Tyr Cys  
 AGA CAA GCA TAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE125-1  
 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 40 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 45 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 50 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

55

SEQ ID NO: EE125-1

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Leu Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT CTA GGA

20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGC AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE125-2

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE125-2

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Leu Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT CTA GGA

50

55

20 25 30  
 Pro Gly Lys Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGA AAA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

5

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

10

## (2) INFORMATION FOR SEQ ID NO: EEE125-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

15

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

20

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

25

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

30

SEQ ID NO: EEE125-3

35

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Leu Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT CTA GGA

40

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

45

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

50

55

## (2) INFORMATION FOR SEQ ID NO: EE131-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE131-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Ser Lys Arg Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGC AAA AGA ATA TCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Arg Ala Thr Arg Ile Ile Gly Asp Ile Arg  
 CCA GGG AGA GCT TTT CGT GCA ACA AGA ATA ATA GGA GAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE131-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment

- (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE131-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Ser Lys Arg Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGT AAA AGA ATA TCT ATA GGA

20 25 30  
 Pro Gly MET Ala Phe Arg Ala Thr Arg Ile Ile Gly Asp Ile Arg  
 CCA GGG ATG GCA TTT CGT GCA ACA AGA ATA ATA GGA GAT ATA AGA

25 35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE131-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE131-3

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Thr Ser Lys Arg Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGC AAA AGA ATA TCT ATA GGA  
 20 25 30  
 10 Pro Gly Arg Ala Phe Arg Ala Thr Arg Ile Ile Gly Asp Ile Arg  
 CCA GGG AGA GCA TTT CGT GCA ACA AGA ATA ATA GGA GAT ATA AGA  
 35  
 15 Gln Ala His Cys  
 CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EEE149-1  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EEE149-1

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE149-2
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE149-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE149-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE149-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EEE159-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment



- (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE159-1

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

25 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EEE159-2  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE159-2

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA CCT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE159-3

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE159-3

1 5 10 15  
 45 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
  
 20 25 30  
 50 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile

55

35  
AGA CAA GCA CAT TGT  
Arg Gln Ala His Cys

5

- (2) INFORMATION FOR SEQ ID NO: EE164-1
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

10

15

20

25

SEQ ID NO: EE164-1

30

1 5 10 15  
Cys Thr Arg Pro Ser Asn Asn Thr Ser Lys Gly Ile His Ile Gly  
TGT ACA AGA CCC AGC AAC AAT ACA AGC AAA GGT ATA CAT ATA GGA

35

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asn Ile Ile Gly Asn Ile  
CCA GGG AGA GCA TTT TAT ACA ACA GGA AAT ATA ATA GGA AAT ATA

40

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

45

- (2) INFORMATION FOR SEQ ID NO: EE164-2
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid

50

55

- (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE164-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Ser Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGC AGA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asn Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA AAT ATA ATA GGA GAT ATA

35  
 Arg Arg Ala His Cys  
 AGA CGA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EEE164-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE164-3

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA

25 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE179-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE179-1

5           1                   5                   10                   15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10                   20                   25                   30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

15                   35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAC TGT

20   (2)    INFORMATION FOR SEQ ID NO: EE179-2  
          (i)    SEQUENCE CHARACTERISTICS:  
                   (A)    LENGTH: 105  
                   (B)    TYPE: Nucleic Acid  
                   (C)    STRANDEDNESS: Single  
                   (D)    TOPOLOGY: Linear  
 25           (ii)   KIND: cDNA to genomic RNA  
              (ii)   KIND (if peptide or protein):  
                   (A)    SEQUENCE ASSEMBLY METHOD: Overlap  
                   (B)    FRAGMENT TYPE: Internal Fragment  
 30           (C)    HYPOTHETICAL: \_\_\_\_\_  
              (iii)   ORIGINAL SOURCE: HIV  
                   (E)    INDIVIDUAL ISOLATE: \_\_\_\_\_  
              (iv)   IMMEDIATE SOURCE:  
                   (C)    CLONE: \_\_\_\_\_  
 35           (v)    POSITION IN GENOME: Within Env Gene  
              (vi)   PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
                   determinant  
              (viii)   SEQUENCE DESCRIPTION:

SEQ ID NO: EE179-2

45           1                   5                   10                   15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAC TGT

- (2) INFORMATION FOR SEQ ID NO: EE179-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE179-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAC TGT

[illegible]

56



- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE181-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GCG AGA GCA TTT TAT ACA ACG GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE181-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE181-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAT AAT ACA AGA AAA AGT ATA CAT ATA GGA  
 20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gly Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACG GGA GGA ATA ATA GGA GAT ATA  
 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE211-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE211-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC GAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EEE211-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EEE211-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Ser Leu Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA TCT CTA GGA

20 25 30  
 Pro Gly Ser Ala Ile Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGT GCA ATT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE215-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA

## (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

## (v) POSITION IN GENOME: Within Env Gene

## (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

## (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE215-1

1 5 10 15  
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA CAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCG CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE215-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

15  
 SEQ ID NO: EE215-2

1 5 10 15  
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 20 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 25 CCA GGC AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

30 35  
 Arg Gln Ala His Cys  
 30 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE215-3
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE215-3

5           1                           5                           10                           15  
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10                           20                           25                           30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

15                           35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

20   (2)    INFORMATION FOR SEQ ID NO: EEE217-1  
           (i)    SEQUENCE CHARACTERISTICS:  
                 (A)    LENGTH: 105  
                 (B)    TYPE: Nucleic Acid  
                 (C)    STRANDEDNESS: Single  
                 (D)    TOPOLOGY: Linear  
           (ii)   KIND: cDNA to genomic RNA  
           (ii)   KIND (if peptide or protein):  
                 (A)    SEQUENCE ASSEMBLY METHOD: Overlap  
                 (B)    FRAGMENT TYPE: Internal Fragment  
                 (C)    HYPOTHETICAL: \_\_\_\_\_  
           (iii)   ORIGINAL SOURCE: HIV  
                 (E)    INDIVIDUAL ISOLATE: \_\_\_\_\_  
           (iv)   IMMEDIATE SOURCE:  
                 (C)    CLONE: \_\_\_\_\_  
           (v)    POSITION IN GENOME: Within Env Gene  
           (vi)   PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
   determinant  
           (viii)  SEQUENCE DESCRIPTION:

SEQ ID NO: EEE217-1

45           1                           5                           10                           15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE217-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE217-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE228-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA

## (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

## (v) POSITION IN GENOME: Within Env Gene

## (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

## (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE228-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE228-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA



- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE228-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA  
 20  
 20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA CAT ATA  
 25  
 30 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT  
 30

(2) INFORMATION FOR SEQ ID NO: EE228-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE228-3

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE229-1

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE229-1

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AGA AGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg  
 CCA GGG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE229-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE229-2

1 5 10 15  
 Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg  
 CCA GGG AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE229-3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE229-3

1 5 10 15  
 Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg  
 CCA GGG AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EEE244-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

15

SEQ ID NO: EE244-1

1 5 10 15  
 20 Cys Thr Arg Pro Asn Asn Ile Lys Ile Arg Ser Ile His Ile  
 TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

20 25 30  
 25 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg  
 GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

35  
 30 Gln Ala Tyr Cys  
 CAA GCA TAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE244-2  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

55

SEQ ID NO: EE244-2

```

      1           5           10           15
5   Cys Thr Arg Pro Asn Asn Asn Ile Lys Ile Arg Ser Ile His Ile
   TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

      20           25           30
10  Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg
   GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

      35
15  Gln Ala Tyr Cys
   CAA GCA TAT TGT

```

```

(2)  INFORMATION FOR SEQ ID NO: EE244-3
20  (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 102
      (B)  TYPE: Nucleic Acid
      (C)  STRANDEDNESS: Single
      (D)  TOPOLOGY: Linear
25  (ii)  KIND: cDNA to genomic RNA
      (ii)  KIND (if peptide or protein):
      (A)  SEQUENCE ASSEMBLY METHOD: Overlap
      (B)  FRAGMENT TYPE: Internal Fragment
      (C)  HYPOTHETICAL: _____
30  (iii)  ORIGINAL SOURCE: HIV
      (E)  INDIVIDUAL ISOLATE: _____
      (iv)  IMMEDIATE SOURCE:
      (C)  CLONE: _____
      (v)  POSITION IN GENOME: Within Env Gene
35  (vi)  PROPERTIES OF SEQUENCE: Expresses conserved antigenic
      determinant
      (viii) SEQUENCE DESCRIPTION:

```

40 SEQ ID NO: EE244-3

```

      1           5           10           15
45  Cys Thr Arg Pro Asn Asn Asn Ile Lys Ile Arg Ser Ile His Ile
   TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

```

50

55

20 25 30  
 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg  
 GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

5

35  
 Gln Ala Tyr Cys  
 CAA GCA TAT TGT

10

## (2) INFORMATION FOR SEQ ID NO: EE289-1

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

20

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

25

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

30

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE289-1

35

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

40

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACT ACA GGA GAA ATA ATA GGA GAT ATA

45

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

50

55

## (2) INFORMATION FOR SEQ ID NO: EE289-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA

## (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

## (v) POSITION IN GENOME: Within Env Gene

## (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

## (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE289-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACT ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE290-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA



- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE290-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Leu Gly  
 20 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA GGC

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 25 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 30 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE293-1
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE293-1

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE293-2

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 35 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE293-2

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE293-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE293-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE295-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE295-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Lys Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA AAA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE295-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE295-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA  
 20  
 20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Lys Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA AAA GAC ATA ATA GGA GAT ATA  
 25  
 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT  
 30

(2) INFORMATION FOR SEQ ID NO: EE297-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE297-1

```

      1           5           10           15
5   Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
    TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

      20           25           30
10  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
    CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

      35
15  Arg Gln Ala His Cys
    AGA CAA GCA CAT TGT

```

```

(2)  INFORMATION FOR SEQ ID NO: EE297-2
20  (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 105
      (B)  TYPE: Nucleic Acid
      (C)  STRANDEDNESS: Single
      (D)  TOPOLOGY: Linear
25  (ii) KIND: cDNA to genomic RNA
      (ii) KIND (if peptide or protein):
      (A)  SEQUENCE ASSEMBLY METHOD: Overlap
      (B)  FRAGMENT TYPE: Internal Fragment
      (C)  HYPOTHETICAL: _____
30  (iii) ORIGINAL SOURCE: HIV
      (E)  INDIVIDUAL ISOLATE: _____
      (iv) IMMEDIATE SOURCE:
      (C)  CLONE: _____
      (v)  POSITION IN GENOME: Within Env Gene
35  (vi)  PROPERTIES OF SEQUENCE: Expresses conserved antigenic
      determinant
      (viii) SEQUENCE DESCRIPTION:

```

40 SEQ ID NO: EE297-2

```

      1           5           10           15
45  Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly
    TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

```

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE297-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE297-3

1 5 10 15  
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ATA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE304-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE304-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE304-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA



- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE304-2

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly			
TGT ACA AGA CCC AAC AAC AAT ACA AGG AGA AGT ATA AAT ATA GGA			
20	25	30	
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile			
CCA GCG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA			
35			
Arg Gln Ala His Cys			
AGA CAA GCA CAT TGT			

(2) INFORMATION FOR SEQ ID NO: EE304-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

EP 0 471 407 A2

SEQ ID NO: EE304-3

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AGA AGT ATA AAT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT  
  
 20  
  
 25  
  
 30  
  
 35  
  
 40  
  
 45  
  
 50  
  
 55

## (2) INFORMATION FOR SEQ ID NO: EE308-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL

ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE308-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGC AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE308-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE308-2

```

      1           5           10           15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

      20           25           30
Pro Gly Arg Pro Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
CCA GGC AGA CCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

      35
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT

```

(2) INFORMATION FOR SEQ ID NO: EE310-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE310-1

1 5 10 15  
 5 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACC AGA AGA GGT ATA CAT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE310-2  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE310-2

1 5 10 15  
 45 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE310-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE310-3

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE311-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE311-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACC AGA AGA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Ala Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GCT ATA ATA GCA GAT ATA

35  
 Arg Arg Ala Tyr Cys  
 AGA CGA GCA TAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE312-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE312-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Glu Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg  
 CCA GAG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE312-2

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 99  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EEE312-2

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AAA ACT ATA ACT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg  
 CCA GGG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA  
  
 35  
 15 Gln Ala His  
 CAA GCA CAT

(2) INFORMATION FOR SEQ ID NO: EE313-1  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE313-1

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly  
 TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

50

55

20 25 30  
 Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile  
 CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA

35  
 Arg Arg Ala His Cys  
 AGA CGA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE317-1
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE317-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE320-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE320-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGC

## 2) INFORMATION FOR SEQ ID NO: EE320-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 5 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 10 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE320-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 20 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 25 CCA GGC AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

30 35  
 Arg Gln Ala His Cys  
 30 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE322-1

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 99  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 40 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 45 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 50 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE322-1

5           1                   5                   10                   15  
 Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro  
 ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA CCA

10                   20                   25                   30  
 Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg Gln  
 GGG AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA CAA

15                   35  
 Ala His Cys  
 GCA CAT TGT

20   (2)   INFORMATION FOR SEQ ID NO: EE322-2  
       (i)   SEQUENCE CHARACTERISTICS:  
           (A)   LENGTH: 105  
           (B)   TYPE: Nucleic Acid  
           (C)   STRANDEDNESS: Single  
           (D)   TOPOLOGY: Linear  
       (ii)   KIND: cDNA to genomic RNA  
       (ii)   KIND (if peptide or protein):  
           (A)   SEQUENCE ASSEMBLY METHOD: Overlap  
           (B)   FRAGMENT TYPE: Internal Fragment  
           (C)   HYPOTHETICAL: \_\_\_\_\_  
       (iii)   ORIGINAL SOURCE: HIV  
           (E)   INDIVIDUAL ISOLATE: \_\_\_\_\_  
       (iv)   IMMEDIATE SOURCE:  
           (C)   CLONE: \_\_\_\_\_  
       (v)   POSITION IN GENOME: Within Env Gene  
       (vi)   PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
               determinant  
       (viii)   SEQUENCE DESCRIPTION:

40

SEQ ID NO: EE322-2

45           1                   5                   10                   15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GCA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE322-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE322-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE324-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE324-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

20 25 30  
 Leu Gly Arg Thr Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile  
 CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE324-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE324-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Leu Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA GGG

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GCG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Gly Gln Ala His Cys  
 GGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE327-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EE327-1

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE327-2  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE327-2

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Tyr  
 AGA CAA GCA CAT TAT

- (2) INFORMATION FOR SEQ ID NO: EE327-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE327-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE345-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-1

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAT AAT ACA AGA AAA GGT ATA CAT ATA GGG

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACG GGA GAG ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE345-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-2

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAT AAT ACA AGA AAA GGT ATA CAT ATA GGG

20 25 30  
 Pro Gly Arg Ala Phe Phe Thr Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TTT ACA ACA GGA GAA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE345-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-3

1 5 10 15  
 5 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAT AAT ACA AGA AAA AGT ATA CAT ATA GGG  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACG GGA GAG ATA ACA GGA CAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE356-1  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE356-1

1 5 10 15  
 45 Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ATA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE356-2
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE356-2

1 5 10 15  
 Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ATA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE356-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE356-3

1 5 10 15  
 Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ATA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE359-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE359-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA ACT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE359-2

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EE359-2

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC GAC AAT ACA AGA AGA AGT ATA AAT ATA GGA  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAC ATA ATA GGA CAT ATA  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE359-3  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE359-3

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC GAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCC TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE360-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE360-1

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala  
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE360-2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (iii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE360-2

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala  
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE360-3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE360-3

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala  
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE367-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE367-1

```

      1           5           10           15
5   Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly
    TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

      20           25           30
10  Leu Gly Arg Thr Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile
    CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA CAT ATA

      35
15  Arg Gln Ala His Cys
    AGA CAA GCA CAT TGT

```

```

(2)  INFORMATION FOR SEQ ID NO: EE367-2
20  (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 105
      (B)  TYPE: Nucleic Acid
      (C)  STRANDEDNESS: Single
      (D)  TOPOLOGY: Linear
25  (ii) KIND: cDNA to genomic RNA
      (ii) KIND (if peptide or protein):
      (A)  SEQUENCE ASSEMBLY METHOD: Overlap
      (B)  FRAGMENT TYPE: Internal Fragment
      (C)  HYPOTHETICAL: _____
30  (iii) ORIGINAL SOURCE: HIV
      (E)  INDIVIDUAL ISOLATE: _____
      (iv) IMMEDIATE SOURCE:
      (C)  CLONE: _____
      (v)  POSITION IN GENOME: Within Env Gene
35  (vi)  PROPERTIES OF SEQUENCE: Expresses conserved antigenic
      determinant
      (viii) SEQUENCE DESCRIPTION:

```

40 SEQ ID NO: EE367-2

```

      1           5           10           15
45  Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly
    TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

```

50

55

20 25 30  
 Leu Gly Arg Thr Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile  
 CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE367-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE367-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA

20 25 30  
 Leu Gly Arg Thr Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile  
 CTA GGG AGG ACA TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE370-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
  - (B) FRAGMENT TYPE: Internal Fragment
  - (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE370-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE370-2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE370-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE370-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EE370-3

```

      1           5           10           15
5  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
   TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

      20           25           30
10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
   CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

      35
15 Arg Gln Ala His Cys
   AGA CAA GCA CAT TGT

```

```

(2)  INFORMATION FOR SEQ ID NO: EE374-1
20  (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 105
      (B)  TYPE: Nucleic Acid
      (C)  STRANDEDNESS: Single
      (D)  TOPOLOGY: Linear
25  (ii) KIND: cDNA to genomic RNA
      (ii) KIND (if peptide or protein):
      (A)  SEQUENCE ASSEMBLY METHOD: Overlap
      (B)  FRAGMENT TYPE: Internal Fragment
      (C)  HYPOTHETICAL: _____
30  (iii) ORIGINAL SOURCE: HIV
      (E)  INDIVIDUAL ISOLATE: _____
      (iv) IMMEDIATE SOURCE:
      (C)  CLONE: _____
      (v)  POSITION IN GENOME: Within Env Gene
35  (vi)  PROPERTIES OF SEQUENCE: Expresses conserved antigenic
      determinant
      (viii) SEQUENCE DESCRIPTION:

```

40 SEQ ID NO: EE374-1

```

      1           5           10           15
45 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
   TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

```

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE374-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE374-2

1 5 10 15  
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE374-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE374-3

1 5 10 15  
 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE378-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE378-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE378-2

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE378-2

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE378-3  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

40 SEQ ID NO: EE378-3

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GCA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE380-1
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE380-1

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE380-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE380-2

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GCA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE397-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE397-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CAC ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala Tyr Cys  
 AGA CAA GCA TAT TGC

(2) INFORMATION FOR SEQ ID NO: EE399-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EE399-1

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE399-2  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE399-2

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA CAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE399-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE399-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE405-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE405-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Thr Thr Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGA ATA ACT ACG GGA

20 25 30  
 Pro Gly Arg Val Tyr Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCG GGG AGA GTA TAT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Lys Ala His Cys  
 AGA AAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE405-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 5 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 10 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE405-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Thr Thr Gly  
 20 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGA ATA ACT ACG GGA  
 20 25 30  
 Pro Gly Arg Val Tyr Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 25 CCG GGG AGA GTA TAT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA  
 30 35  
 Arg Lys Ala His Cys  
 30 AGA AAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE405-3

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 40 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 45 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 50 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE405-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Lys Ile Thr Thr Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AAA ATA ACT ACG GGA  
 20 25 30  
 Pro Gly Arg Val Tyr Tyr Thr Thr Gly Glu Ile Ile Glu Asp Val  
 CCG GGG AGA GTA TAT TAT ACA ACA GGA GAA ATA ATA GAA GAT GTA  
 35  
 Arg Lys Ala His Cys  
 AGA AAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE505-1  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE505-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

50

55

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Thr Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAT ATA ACA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE505-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE505-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly  
TGT ACA AGG CCC AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Thr Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAT ATA ACA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE505-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE505-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly  
 TGT ACA AGG CCC AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Thr Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAT ATA ACA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 ACA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE507-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE507-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE509-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EE509-1

1 5 10 15  
 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA GGT ATA CAT ATA GGA  
  
 20 25 30  
 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCG GCG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA  
  
 35  
 15 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE509-2  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 25 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 30 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 35 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE509-2

1 5 10 15  
 45 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA GGT ATA CAT ATA GGA

50

55

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCG GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE510-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA

## (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

## (v) POSITION IN GENOME: Within Env Gene

## (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

## (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE510-1

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGT AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT

20 25 30  
 Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg  
 CCA GGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE510-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE510-2

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AGT AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT

20 25 30  
 Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg  
 CCA GGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA AGA

35  
 Gln Ala His Cys  
 CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE510-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

- (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 5 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 10 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic  
 determinant  
 (viii) SEQUENCE DESCRIPTION:

15 SEQ ID NO: EE510-3

1 5 10 15  
 20 Cys Thr Arg Leu Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CTC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT

20 25 30  
 25 Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg  
 CCA GGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA AGA

35  
 30 Gln Ala His Cys  
 CAG GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE520-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE520-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE520-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE520-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

25 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE520-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE520-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  
 20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA  
 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGC

(2) INFORMATION FOR SEQ ID NO: EE528-1  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE528-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACG AGG AGA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Val Tyr Ala Thr Asp Lys Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA GTT TAT GCA ACA GAT AAA ATA ATA GCA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE528-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE528-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACC AGG AGA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Val Tyr Ala Thr Asp Lys Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA GTT TAT GCA ACA GAT AAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT



## (2) INFORMATION FOR SEQ ID NO: EE528-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE528-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACG AGG AGA GGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Val Tyr Ala Thr Asp Lys Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA GTT TAT GCA ACA GAT AAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE529-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE529-1

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE529-2

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE529-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGA CCT AAC AAT AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCG GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE533-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE533-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- 5
- (2) INFORMATION FOR SEQ ID NO: EE533-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:
- 10
- 15
- 20
- 25

SEQ ID NO: EE533-2

30

1	5	10	15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly			
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA			

35

20	25	30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile		
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA		

40

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- 45
- (2) INFORMATION FOR SEQ ID NO: EE533-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- 50
- 55

- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE533-3

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE535-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene

- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE535-1

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GCA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE535-2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE535-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE543-1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE543-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE543-2
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE543-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE543-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment



- (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE543-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
 TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA CAT ATA

25 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE558-1  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE558-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGC

## (2) INFORMATION FOR SEQ ID NO: EE558-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) KIND: cDNA to genomic RNA

## (ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

## (v) POSITION IN GENOME: Within Env Gene

## (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant

## (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE558-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Leu Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA GGG

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGC

5

## (2) INFORMATION FOR SEQ ID NO: EE558-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10

## (ii) KIND: cDNA to genomic RNA

## (iii) KIND (if peptide or protein):

15

## (A) SEQUENCE ASSEMBLY METHOD: Overlap

## (B) FRAGMENT TYPE: Internal Fragment

## (C) HYPOTHETICAL: \_\_\_\_\_

## (iii) ORIGINAL SOURCE: HIV

## (E) INDIVIDUAL ISOLATE: \_\_\_\_\_

20

## (iv) IMMEDIATE SOURCE:

## (C) CLONE: \_\_\_\_\_

## (v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

25

## (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE558-3

30

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Leu Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA GGG

35

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

40

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

45

## (2) INFORMATION FOR SEQ ID NO: EE594-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid

50

55

- (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE594-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr MET Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA ATG AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE594-2

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:

(v) POSITION IN GENOME: Within Env Gene  
(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant  
(viii) SEQUENCE DESCRIPTION:

10

15

20

25

30

35

40

5

55

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr MET Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA ATG AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE628-1
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
    - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE628-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly  
 TGT ACA AGA CCC AAC AAT AAT ACA AGA AAA GGT ATA CAT ATG GGA

20 25 30  
 Pro Gly Lys Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile  
 CCA GGG AAA GCA TTT TAT GCA ACA GGG GAC ATA ATA GGA AAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- 5  
10  
15  
20  
25
- (2) INFORMATION FOR SEQ ID NO: EE628-2
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE628-2

30

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA

35

20 25 30  
Pro Gly Lys Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile  
CCA GGG AAA GCA TTT TAT GCA ACA GGG GAC ATA ATA GGA AAT ATA

40

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- 45
- (2) INFORMATION FOR SEQ ID NO: EE628-3
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- 50
- 55

- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE628-3

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA

25 30 35  
Pro Gly Lys Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile  
CCA GGG AAA GCA TTT TAT GCA ACA GGG GAC ATA ATA GCA AAT ATA

30 35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE639-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_



- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE639-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly  
 TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

20 25 30  
 Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile  
 CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA

35  
 Arg Arg Ala His Cys  
 AGA CGA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE639-2
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE639-2

(2) INFORMATION FOR SEQ ID NO: EE639-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE639-3

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA CCA ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

154

EP 0 471 407 A2

1 5 10 15  
Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly  
TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

20 25 30  
Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile  
CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA

35  
Arg Arg Ala His Cys  
AGA CGA GCA CAT TGT

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

5

## (2) INFORMATION FOR SEQ ID NO: EE660-1

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(iii) KIND (if peptide or protein):

- 15 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

20

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

25

SEQ ID NO: EE660-1

30

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA ACT ATA CCT ATA GGA

35

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Val Ile Gly Asp Ile  
CCA GGA AGA GCA TTT TAT ACA ACA GGA GAT GTA ATA GGA GAT ATA

40

35  
Arg Gln Ala Arg Cys  
AGA CAA GCA CGT TGT

45

## (2) INFORMATION FOR SEQ ID NO: EE660-2

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single

50

55

- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE660-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Ala Ile Ile Gly Asp Ile  
CCA GGC AGA GCA TTC TAT GCA ACA GGA GCC ATA ATA GCA GAT ATA

30 35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE661-1

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_

- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE661-1

```

1           5           10           15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

15
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA CAT ATA

20
Arg Gln Ala His Cys
AGA CAA GCA CAT TGT
  
```

- (2) INFORMATION FOR SEQ ID NO: EE661-2
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE661-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE661-3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE661-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Ser Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA TCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Phe Thr Thr Gly Gln Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TTT ACA ACA GGA CAA ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- 5  
(2) INFORMATION FOR SEQ ID NO: EE663-1  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
10 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) KIND: cDNA to genomic RNA  
(iii) KIND (if peptide or protein):  
(A) SEQUENCE ASSEMBLY METHOD: Overlap  
15 (B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_  
(iii) ORIGINAL SOURCE: HIV  
(E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
(iv) IMMEDIATE SOURCE:  
20 (C) CLONE: \_\_\_\_\_  
(v) POSITION IN GENOME: Within Env Gene  
(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant  
(viii) SEQUENCE DESCRIPTION:

25  
SEQ ID NO: EE663-1

30  
1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly  
TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA

35  
20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

40  
35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- 45  
(2) INFORMATION FOR SEQ ID NO: EE663-2  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
50 (C) STRANDEDNESS: Single

- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE663-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE663-3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_



- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE663-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Ile Lys Ser Ile Thr Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA ATA AAA AGT ATA ACT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE665-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE665-1

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA CAA ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE665-2

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) KIND: cDNA to genomic RNA  
(ii) KIND (if peptide or protein):  
(A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_  
(iii) ORIGINAL SOURCE: HIV  
(E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
(iv) IMMEDIATE SOURCE:  
(C) CLONE: \_\_\_\_\_  
(v) POSITION IN GENOME: Within Env Gene  
(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant  
(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE665-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Ile Ile Gly Asp Ile  
CCA GGG AGA GCA TTT TAT GCA ACA GGA CAA ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

5

## (2) INFORMATION FOR SEQ ID NO: EE665-3

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) KIND: cDNA to genomic RNA  
(ii) KIND (if peptide or protein):  
15 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_  
(iii) ORIGINAL SOURCE: HIV  
(E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
20 (iv) IMMEDIATE SOURCE:  
(C) CLONE: \_\_\_\_\_  
(v) POSITION IN GENOME: Within Env Gene  
(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant  
25 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE665-3

30

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly  
TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA

35

20 25 30  
Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Ile Ile Gly Asp Ile  
CCA GGC AGA GCA TTT TAT GCA ACA GGA CAA ATA ATA GGA GAT ATA

40

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

45

## (2) INFORMATION FOR SEQ ID NO: EE667-1

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single

55

- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE667-1

1 5 10 15  
Cys Thr Arg Pro Asn Asn Thr Arg Lys Arg Ile Thr Thr Gly  
TGT ACA ACA CCC AAC AAC AAT ACA AGA AAA AGA ATA ACT ACG GGA

20 25 30  
Pro Gly Arg Val Tyr Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
CCG GGG AGA GTA TAT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA

30 35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE667-2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_

- (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE667-2

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAC TGT

(2) INFORMATION FOR SEQ ID NO: EE667-3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE667-3

1 5 10 15  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala  
 TGC ACA AGG CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAC TGT

## (2) INFORMATION FOR SEQ ID NO: EE669-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE669-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCT AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Ile Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA ATT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE669-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE669-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCT AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Ile Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGG AGA GCA ATT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE669-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment

- (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE669-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCT AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile  
 CCA GGC AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GCA GAT ATA

25 35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

(2) INFORMATION FOR SEQ ID NO: EE1476-1

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:



SEQ ID NO: EE1476-1

5           1                   5                   10                   15  
 Cys Thr Arg Pro Tyr Asn Asn Ile Lys Ile Arg Ser Ile His Ile  
 TGT ACA AGG CCC TAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

10                   20                   25                   30  
 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg  
 GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA

15                   35  
 Gln Ala Tyr Cys  
 CAA GCA TAT TGT

20       (2)       INFORMATION FOR SEQ ID NO: EE3032-1  
           (i)       SEQUENCE CHARACTERISTICS:  
                   (A)       LENGTH: 105  
                   (B)       TYPE: Nucleic Acid  
                   (C)       STRANDEDNESS: Single  
                   (D)       TOPOLOGY: Linear  
           (ii)       KIND: cDNA to genomic RNA  
           (ii)       KIND (if peptide or protein):  
                   (A)       SEQUENCE ASSEMBLY METHOD: Overlap  
                   (B)       FRAGMENT TYPE: Internal Fragment  
                   (C)       HYPOTHETICAL: \_\_\_\_\_  
           (iii)       ORIGINAL SOURCE: HIV  
                   (E)       INDIVIDUAL ISOLATE: \_\_\_\_\_  
           (iv)       IMMEDIATE SOURCE:  
                   (C)       CLONE: \_\_\_\_\_  
           (v)       POSITION IN GENOME: Within Env Gene  
           (vi)       PROPERTIES OF SEQUENCE: Expresses conserved  
   antigenic determinant  
           (viii)       SEQUENCE DESCRIPTION:

SEQ ID NO: EE3032-1

45           1                   5                   10                   15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGG CCC AAT AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

50                   20                   25                   30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

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35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE3032-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
(B) FRAGMENT TYPE: Internal Fragment  
(C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE3032-2

1 5 10 15  
Cys Thr Arg Pro Asn Asn Thr Arg Lys Gly Ile His MET Gly  
TGT ACA AGG CCC AAT AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE3032-3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single

- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene
- (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant
- (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE3032-3

1 5 10 15  
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
TGT ACA AGG CCC AAT AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile  
CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

30 35  
Arg Gln Ala His Cys  
AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EEE6405-1
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) KIND: cDNA to genomic RNA
- (ii) KIND (if peptide or protein):
- (A) SEQUENCE ASSEMBLY METHOD: Overlap
- (B) FRAGMENT TYPE: Internal Fragment
- (C) HYPOTHETICAL: \_\_\_\_\_
- (iii) ORIGINAL SOURCE: HIV
- (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
- (iv) IMMEDIATE SOURCE:
- (C) CLONE: \_\_\_\_\_
- (v) POSITION IN GENOME: Within Env Gene

20 25 30  
 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile MET Gly Asp Ile  
 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATG GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE6405-3
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) KIND: cDNA to genomic RNA
  - (ii) KIND (if peptide or protein):
    - (A) SEQUENCE ASSEMBLY METHOD: Overlap
    - (B) FRAGMENT TYPE: Internal Fragment
    - (C) HYPOTHETICAL: \_\_\_\_\_
  - (iii) ORIGINAL SOURCE: HIV
  - (E) INDIVIDUAL ISOLATE: \_\_\_\_\_
  - (iv) IMMEDIATE SOURCE:
    - (C) CLONE: \_\_\_\_\_
  - (v) POSITION IN GENOME: Within Env Gene
  - (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
  - (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6405-3

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA AGT ATA CCT ATA GGA

20 25 30  
 Pro Arg Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile  
 CCA AGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE6636-1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_

(iii) ORIGINAL SOURCE: HIV

(E) INDIVIDUAL ISOLATE: \_\_\_\_\_

(iv) IMMEDIATE SOURCE:

(C) CLONE: \_\_\_\_\_

(v) POSITION IN GENOME: Within Env Gene

(vi) PROPERTIES OF SEQUENCE: Expresses conserved  
antigenic determinant

(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6636-1

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## (2) INFORMATION FOR SEQ ID NO: EE6636-2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) KIND: cDNA to genomic RNA

(ii) KIND (if peptide or protein):

- (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment

- (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6636-2

1 5 10 15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

- (2) INFORMATION FOR SEQ ID NO: EE6636-3  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear  
 (ii) KIND: cDNA to genomic RNA  
 (ii) KIND (if peptide or protein):  
 (A) SEQUENCE ASSEMBLY METHOD: Overlap  
 (B) FRAGMENT TYPE: Internal Fragment  
 (C) HYPOTHETICAL: \_\_\_\_\_  
 (iii) ORIGINAL SOURCE: HIV  
 (E) INDIVIDUAL ISOLATE: \_\_\_\_\_  
 (iv) IMMEDIATE SOURCE:  
 (C) CLONE: \_\_\_\_\_  
 (v) POSITION IN GENOME: Within Env Gene  
 (vi) PROPERTIES OF SEQUENCE: Expresses conserved  
 antigenic determinant  
 (viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE6636-3

5                   1                                   5                                   10                                   15  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly  
 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

10                                   20                                   25                                   30  
 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile  
 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

15                                   35  
 Arg Gln Ala His Cys  
 AGA CAA GCA CAT TGT

## 20 Claims

1. An antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, comprising an antigenic conjugate of the formula

25 (PND)<sub>n</sub>~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

30 PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n indicates the number of polypeptides of PND covalently linked to Omp and is 1-50;

~ indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria,

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length;

35 said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing with the exception of sequence nos. EE90-1, EE90-2, EE90-3, EE312-1, EE360-1, EE360-2, EE360-3, EE667-3 and EE6405-3.

- 40 2. The antigenic conjugate of claim 1 wherein X is proline.
3. The antigenic conjugate of claim 1 wherein the covalent linkage between PND and Omp consists essentially of a bigeneric spacer.
- 45 4. The antigenic conjugate of claims 1-3, in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.
5. The antigenic conjugate of claims 1-3, wherein said Omp is derived from Neisseria meningitidis.
- 50 6. A cocktail of antigenic conjugates consisting essentially of a mixture of more than one molecular species of the antigenic conjugates of claims 1-3.
7. An AIDS vaccine comprising an antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, said conjugate of the formula

(PND)<sub>n</sub>~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n indicates the number of polypeptides of PND covalently linked to Omp and is 1-50;

~ indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria;

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length;

said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing;

said conjugate mixed with a suitable immunological adjuvant, carrier or vector, said vaccine to be used pre- and post-exposure to prevent or treat HIV infection or disease, said vaccine capable of eliciting specific HIV neutralizing antibodies.

8. The AIDS vaccine of claim 7 wherein X is proline.

9. The AIDS vaccine of claim 7 wherein the covalent linkage between PND and Omp consists essentially of a bigeneric spacer.

10. The AIDS vaccine of claims 7-9 in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.

11. The AIDS vaccine of claims 7-9, wherein said Omp is derived from Neisseria meningitidis.

12. The AIDS vaccine of claim 7-9 comprising a cocktail of said antigenic conjugates, said cocktail consisting essentially of a mixture of more than one molecular species of said antigenic conjugates.

13. A pharmaceutical composition comprising an antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, said antigenic conjugate of the formula

(PND)<sub>n</sub>~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n indicates the number of polypeptides of PND covalently linked to Omp and is 1-50;

~ indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria,

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length;

said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing;

said conjugate mixed with a suitable immunological adjuvant, said composition useful as a vaccine capable of producing specific HIV neutralizing antibody in mammals.

14. The composition of claim 13 wherein X is proline.

15. The composition of claim 13 wherein the covalent linkage between PND and Omp consists essentially of a bigeneric spacer.

16. The composition of claims 13-15, in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.

17. The composition of claims 13-15, wherein said Omp is derived from Neisseria meningitidis.

18. A pharmaceutical composition containing a cocktail of antigenic conjugates consisting essentially of a mixture of more than one molecular species of the antigenic conjugates of claims 13-15.



19. The use of a conjugate as claimed in claim 1 for the preparation of a medicament for vaccinating against AIDS or ARC.
- 5 20. The use of a conjugate as claimed in claim 2 for the preparation of a medicament for vaccinating against AIDS or ARC.
21. The use of a conjugate as claimed in claim 3 for the preparation of a medicament for vaccinating against AIDS or ARC.
- 10 22. The use of a conjugate as claimed in claim 1 together with any of the antivirals, immunomodulators or anti-infectives of Table I for the preparation of a medicament for vaccinating against AIDS or ARC.
23. The use as claimed in claim 19 or 20 wherein the Omp is derived from Neisseria meningitidis.
- 15 24. The use of a conjugate as claimed in claim 1 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
25. The use of a conjugate as claimed in claim 2 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
- 20 26. The use of a conjugate as claimed in claim 3 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
- 25 27. The use of a conjugate as claimed in claim 1 together with any of the antivirals, immunomodulators or anti-infectives of Table I for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
28. The use as claimed in claim 24 or 25 wherein the Omp is derived from Neisseria meningitidis.

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